

SEQUENCE LISTING

<110> Jukka T. SALONEN et al.

<120> METHOD FOR DETECTING THE RISK OF CARDIOVASCULAR DISEASES SUCH AS ACUTE MYOCARDIAL INFARCTION AND CORONARY HEART DISEASE BY ANALYSING DEFENSIN

<130> 0933-0279PUS1

<140> US 10/586,312

<141> 2006-07-14

<160> 56

<170> PatentIn version 3.1

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<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

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<223> Description of Artificial Sequence: PCR primer

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<211> 18

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 <223> Description of Artificial Sequence: PCR primer

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 ctgagtgtgc aggacgag 18

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 <223> Description of Artificial Sequence: PCR primer

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 <211> 736
 <212> DNA
 <213> Homo sapiens

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 caggctgact cctcactccc cacatatcca ctctgtctct ccctcctgca ggtgacccca 180
 gccatgagga ccatcgccat ccttgctgcc attctcctgg tggccctgca ggcccaggct 240
 gagtcactcc aggaaagagc tgatgaggct acaaccaga agcagtctgg ggaagacaac 300
 caggaccttg ctatctcctt tgcaggaaat ggactctctg ctcttagaac ctcaggtagg 360
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 gtcaagtgtg gaaagggtcta cctcacttga gtgactttac ttaatcttcc tggaccttga 480
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acactgacta gttcttttga gatctaaatg ggcagactta gttatataga gagtgtttta	660
ctttgtccat tggaaaagct tttagaacct agagaggaac ctataggtgt gttttgatgt	720
aggctaatag gcttga	736

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 <212> DNA
 <213> Homo sapiens

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caggctgact cctcactccc cacatatcca ctctgctct cctcctgca ggtgaccca	180
gccatgagga ccatcgccat ccttgctgcc attctcctgg tggccctgca ggcccaggct	240
gagtcactcc aggaaagagc tgatgaggct acaaccaga agcagtctgg ggaagacaac	300
caggaccttg ctatctcctt tgcaggaaat ggactctctg ctcttagaac ctcaggtagg	360
agacatcaat cttgcacatc tgcaaaatct agaaaaaag gattggagaa aggatctgga	420
gtcaagtgtg gaaagggtcta cctcacttga gtgactttac ttaatcttcc tggaccttga	480
ttttctcatc tataaattaa tcagtgagaa ccaaataaat ctaaaagatt ttcttttttc	540
taagactttc agctccaaga tatttctgtg aaatttgcta cttttaagat agaaagagct	600
acactgacta gttcttttga gatctaaatg ggcagactta gttatataga gagtgtttta	660
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 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR primer

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<210> 10
 <211> 19
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<220>
 <223> Description of Artificial Sequence: PCR primer

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 tcaagcctat tagcctaca 19

 <210> 11
 <211> 20
 <212> DNA
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 <220>
 <223> Description of Artificial Sequence: PCR primer

 <400> 11
 gacaacctca atgctctgct 20

 <210> 12
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: PCR primer

 <400> 12
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 <210> 13
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 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Snapshot primer

 <400> 13
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 <223> Snapshot primer

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<211> 45
 <212> DNA
 <213> Artificial Sequence

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 <223> Snapshot primer

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 <213> Artificial Sequence

 <220>
 <223> Snapshot primer

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 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Snapshot primer

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 <211> 60
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 <213> Artificial Sequence

 <220>
 <223> Snapshot primer

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 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Snapshot primer

 <400> 19
 tttttttttt tttgaagacc agccagtgca 30

<210> 20
 <211> 1344
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(1344)
 <223> Coding sequence for variant human ADRA2B gene

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 Met Asp His Gln Asp Pro Tyr Ser Val Gln Ala Thr Ala Ala Ile Ala
 1 5 10 15

gcg gcc atc acc ttc ctc att ctc ttt acc atc ttc ggc aac gct ctg 96
 Ala Ala Ile Thr Phe Leu Ile Leu Phe Thr Ile Phe Gly Asn Ala Leu
 20 25 30

gtc atc ctg gct gtg ttg acc agc cgc tcg ctg cgc gcc cct cag aac 144
 Val Ile Leu Ala Val Leu Thr Ser Arg Ser Leu Arg Ala Pro Gln Asn
 35 40 45

ctg ttc ctg gtg tcg ctg gcc gcc gcc gac atc ctg gtg gcc acg ctc 192
 Leu Phe Leu Val Ser Leu Ala Ala Ala Asp Ile Leu Val Ala Thr Leu
 50 55 60

atc atc cct ttc tcg ctg gcc aac gag ctg ctg ggc tac tgg tac ttc 240
 Ile Ile Pro Phe Ser Leu Ala Asn Glu Leu Leu Gly Tyr Trp Tyr Phe
 65 70 75 80

cgg cgc acg tgg tgc gag gtg tac ctg gcg ctc gac gtg ctc ttc tgc 288
 Arg Arg Thr Trp Cys Glu Val Tyr Leu Ala Leu Asp Val Leu Phe Cys
 85 90 95

acc tcg tcc atc gtg cac ctg tgc gcc atc agc ctg gac cgc tac tgg 336
 Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Trp
 100 105 110

gcc gtg agc cgc gcg ctg gag tac aac tcc aag cgc acc ccg cgc cgc 384
 Ala Val Ser Arg Ala Leu Glu Tyr Asn Ser Lys Arg Thr Pro Arg Arg
 115 120 125

atc aag tgc atc atc ctc act gtg tgg ctc atc gcc gcc gtc atc tcg 432
 Ile Lys Cys Ile Ile Leu Thr Val Trp Leu Ile Ala Ala Val Ile Ser
 130 135 140

ctg ccg ccc ctc atc tac aag ggc gac cag ggc ccc cag ccg cgc ggg 480
 Leu Pro Pro Leu Ile Tyr Lys Gly Asp Gln Gly Pro Gln Pro Arg Gly
 145 150 155 160

cgc ccc cag tgc aag ctc aac cag gag gcc tgg tac atc ctg gcc tcc 528
 Arg Pro Gln Cys Lys Leu Asn Gln Glu Ala Trp Tyr Ile Leu Ala Ser
 165 170 175

agc atc gga tct ttc ttt gct cct tgc ctc atc atg atc ctt gtc tac Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met Ile Leu Val Tyr 180 185 190	576
ctg cgc atc tac ctg atc gcc aaa cgc agc aac cgc aga ggt ccc agg Leu Arg Ile Tyr Leu Ile Ala Lys Arg Ser Asn Arg Arg Gly Pro Arg 195 200 205	624
gcc aag ggg ggg cct ggg cag ggt gag tcc aag cag ccc cga ccc gac Ala Lys Gly Gly Pro Gly Gln Gly Glu Ser Lys Gln Pro Arg Pro Asp 210 215 220	672
cat ggt ggg gct ttg gcc tca gcc aaa ctg cca gcc ctg gcc tct gtg His Gly Gly Ala Leu Ala Ser Ala Lys Leu Pro Ala Leu Ala Ser Val 225 230 235 240	720
gct tct gcc aga gag gtc aac gga cac tcg aag tcc act ggg gag aag Ala Ser Ala Arg Glu Val Asn Gly His Ser Lys Ser Thr Gly Glu Lys 245 250 255	768
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agt tgg gct gcc ctt ccc aac tca ggc cag ggc cag aag gag ggt gtt Ser Trp Ala Ala Leu Pro Asn Ser Gly Gln Gly Gln Lys Glu Gly Val 275 280 285	864
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gag gag tgt gaa ccc cag gca gtg cca gtg tct ccg gcc tca gct tgc Glu Glu Cys Glu Pro Gln Ala Val Pro Val Ser Pro Ala Ser Ala Cys 305 310 315 320	960
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cgt ggc cag gtg ctc ctg ggc agg ggc gtg ggt gct ata ggt ggg cag Arg Gly Gln Val Leu Leu Gly Arg Gly Val Gly Ala Ile Gly Gly Gln 340 345 350	1056
tgg tgg cgt cga agg gcg cac gtg acc cgg gag aag cgc ttc acc ttc Trp Trp Arg Arg Arg Ala His Val Thr Arg Glu Lys Arg Phe Thr Phe 355 360 365	1104
gtg ctg gct gtg gtc att ggc gtt ttt gtg ctc tgc tgg ttc ccc ttc Val Leu Ala Val Val Ile Gly Val Phe Val Leu Cys Trp Phe Pro Phe 370 375 380	1152
ttc ttc agc tac agc ctg ggc gcc atc tgc ccg aag cac tgc aag gtg Phe Phe Ser Tyr Ser Leu Gly Ala Ile Cys Pro Lys His Cys Lys Val 385 390 395 400	1200
ccc cat ggc ctc ttc cag ttc ttc ttc tgg atc ggc tac tgc aac agc	1248

Pro His Gly Leu Phe Gln Phe Phe Phe Trp Ile Gly Tyr Cys Asn Ser
 405 410 415

tca ctg aac cct gtt atc tac acc atc ttc aac cag gac ttc cgc cgt 1296
 Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn Gln Asp Phe Arg Arg
 420 425 430

gcc ttc cgg agg atc ctg tgc cgc ccg tgg acc cag acg gcc tgg tga 1344
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 435 440 445

<210> 21
 <211> 447
 <212> PRT
 <213> Homo sapiens

<400> 21

Met Asp His Gln Asp Pro Tyr Ser Val Gln Ala Thr Ala Ala Ile Ala
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Ala Ala Ile Thr Phe Leu Ile Leu Phe Thr Ile Phe Gly Asn Ala Leu
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Val Ile Leu Ala Val Leu Thr Ser Arg Ser Leu Arg Ala Pro Gln Asn
 35 40 45

Leu Phe Leu Val Ser Leu Ala Ala Ala Asp Ile Leu Val Ala Thr Leu
 50 55 60

Ile Ile Pro Phe Ser Leu Ala Asn Glu Leu Leu Gly Tyr Trp Tyr Phe
 65 70 75 80

Arg Arg Thr Trp Cys Glu Val Tyr Leu Ala Leu Asp Val Leu Phe Cys
 85 90 95

Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Trp
 100 105 110

Ala Val Ser Arg Ala Leu Glu Tyr Asn Ser Lys Arg Thr Pro Arg Arg
 115 120 125

Ile Lys Cys Ile Ile Leu Thr Val Trp Leu Ile Ala Ala Val Ile Ser
 130 135 140

Leu Pro Pro Leu Ile Tyr Lys Gly Asp Gln Gly Pro Gln Pro Arg Gly
 145 150 155 160

Arg Pro Gln Cys Lys Leu Asn Gln Glu Ala Trp Tyr Ile Leu Ala Ser
 165 170 175

Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met Ile Leu Val Tyr
 180 185 190

Leu Arg Ile Tyr Leu Ile Ala Lys Arg Ser Asn Arg Arg Gly Pro Arg
 195 200 205

Ala Lys Gly Gly Pro Gly Gln Gly Glu Ser Lys Gln Pro Arg Pro Asp
 210 215 220

His Gly Gly Ala Leu Ala Ser Ala Lys Leu Pro Ala Leu Ala Ser Val
 225 230 235 240

Ala Ser Ala Arg Glu Val Asn Gly His Ser Lys Ser Thr Gly Glu Lys
 245 250 255

Glu Glu Gly Glu Thr Pro Glu Asp Thr Gly Thr Arg Ala Leu Pro Pro
 260 265 270

Ser Trp Ala Ala Leu Pro Asn Ser Gly Gln Gly Gln Lys Glu Gly Val
 275 280 285

Cys Gly Ala Ser Pro Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu
 290 295 300

Glu Glu Cys Glu Pro Gln Ala Val Pro Val Ser Pro Ala Ser Ala Cys
 305 310 315 320

Ser Pro Pro Leu Gln Gln Pro Gln Gly Ser Arg Val Leu Ala Thr Leu
 325 330 335

Arg Gly Gln Val Leu Leu Gly Arg Gly Val Gly Ala Ile Gly Gly Gln
 340 345 350

Trp Trp Arg Arg Arg Ala His Val Thr Arg Glu Lys Arg Phe Thr Phe
 355 360 365

Val Leu Ala Val Val Ile Gly Val Phe Val Leu Cys Trp Phe Pro Phe
 370 375 380

Phe Phe Ser Tyr Ser Leu Gly Ala Ile Cys Pro Lys His Cys Lys Val
 385 390 395 400

Pro His Gly Leu Phe Gln Phe Phe Phe Trp Ile Gly Tyr Cys Asn Ser
 405 410 415

Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn Gln Asp Phe Arg Arg
 420 425 430

Ala Phe Arg Arg Ile Leu Cys Arg Pro Trp Thr Gln Thr Ala Trp
 435 440 445

<210> 22
 <211> 1353
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(1353)
 <223> Coding sequence for human ADRA2B gene

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 Met Asp His Gln Asp Pro Tyr Ser Val Gln Ala Thr Ala Ala Ile Ala
 1 5 10 15

gcg gcc atc acc ttc ctc att ctc ttt acc atc ttc ggc aac gct ctg 96
 Ala Ala Ile Thr Phe Leu Ile Leu Phe Thr Ile Phe Gly Asn Ala Leu
 20 25 30

gtc atc ctg gct gtg ttg acc agc cgc tcg ctg cgc gcc cct cag aac 144
 Val Ile Leu Ala Val Leu Thr Ser Arg Ser Leu Arg Ala Pro Gln Asn
 35 40 45

ctg ttc ctg gtg tcg ctg gcc gcc gcc gac atc ctg gtg gcc acg ctc 192
 Leu Phe Leu Val Ser Leu Ala Ala Ala Asp Ile Leu Val Ala Thr Leu
 50 55 60

atc atc cct ttc tcg ctg gcc aac gag ctg ctg ggc tac tgg tac ttc 240
 Ile Ile Pro Phe Ser Leu Ala Asn Glu Leu Leu Gly Tyr Trp Tyr Phe
 65 70 75 80

cgg cgc acg tgg tgc gag gtg tac ctg gcg ctc gac gtg ctc ttc tgc 288
 Arg Arg Thr Trp Cys Glu Val Tyr Leu Ala Leu Asp Val Leu Phe Cys
 85 90 95

acc tcg tcc atc gtg cac ctg tgc gcc atc agc ctg gac cgc tac tgg 336
 Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Trp
 100 105 110

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atc aag tgc atc atc ctc act gtg tgg ctc atc gcc gcc gtc atc tcg Ile Lys Cys Ile Ile Leu Thr Val Trp Leu Ile Ala Ala Val Ile Ser 130 135 140	432
ctg ccg ccc ctc atc tac aag ggc gac cag ggc ccc cag ccg cgc ggg Leu Pro Pro Leu Ile Tyr Lys Gly Asp Gln Gly Pro Gln Pro Arg Gly 145 150 155 160	480
cgc ccc cag tgc aag ctc aac cag gag gcc tgg tac atc ctg gcc tcc Arg Pro Gln Cys Lys Leu Asn Gln Glu Ala Trp Tyr Ile Leu Ala Ser 165 170 175	528
agc atc gga tct ttc ttt gct cct tgc ctc atc atg atc ctt gtc tac Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met Ile Leu Val Tyr 180 185 190	576
ctg cgc atc tac ctg atc gcc aaa cgc agc aac cgc aga ggt ccc agg Leu Arg Ile Tyr Leu Ile Ala Lys Arg Ser Asn Arg Arg Gly Pro Arg 195 200 205	624
gcc aag ggg ggg cct ggg cag ggt gag tcc aag cag ccc cga ccc gac Ala Lys Gly Gly Pro Gly Gln Gly Glu Ser Lys Gln Pro Arg Pro Asp 210 215 220	672
cat ggt ggg gct ttg gcc tca gcc aaa ctg cca gcc ctg gcc tct gtg His Gly Gly Ala Leu Ala Ser Ala Lys Leu Pro Ala Leu Ala Ser Val 225 230 235 240	720
gct tct gcc aga gag gtc aac gga cac tcg aag tcc act ggg gag aag Ala Ser Ala Arg Glu Val Asn Gly His Ser Lys Ser Thr Gly Glu Lys 245 250 255	768
gag gag ggg gag acc cct gaa gat act ggg acc cgg gcc ttg cca ccc Glu Glu Gly Glu Thr Pro Glu Asp Thr Gly Thr Arg Ala Leu Pro Pro 260 265 270	816
agt tgg gct gcc ctt ccc aac tca ggc cag ggc cag aag gag ggt gtt Ser Trp Ala Ala Leu Pro Asn Ser Gly Gln Gly Gln Lys Glu Gly Val 275 280 285	864
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gag gag gag gaa gag tgt gaa ccc cag gca gtg cca gtg tct ccg gcc Glu Glu Glu Glu Glu Cys Glu Pro Gln Ala Val Pro Val Ser Pro Ala 305 310 315 320	960
tca gct tgc agc ccc ccg ctg cag cag cca cag ggc tcc cgg gtg ctg Ser Ala Cys Ser Pro Pro Leu Gln Gln Pro Gln Gly Ser Arg Val Leu 325 330 335	1008

gcc acc cta cgt ggc cag gtg ctc ctg ggc agg ggc gtg ggt gct ata 1056
Ala Thr Leu Arg Gly Gln Val Leu Leu Gly Arg Gly Val Gly Ala Ile
340 345 350

ggt ggg cag tgg tgg cgt cga agg gcg cac gtg acc cgg gag aag cgc 1104
Gly Gly Gln Trp Trp Arg Arg Arg Ala His Val Thr Arg Glu Lys Arg
355 360 365

ttc acc ttc gtg ctg gct gtg gtc att ggc gtt ttt gtg ctc tgc tgg 1152
Phe Thr Phe Val Leu Ala Val Val Ile Gly Val Phe Val Leu Cys Trp
370 375 380

ttc ccc ttc ttc ttc agc tac agc ctg ggc gcc atc tgc ccg aag cac 1200
Phe Pro Phe Phe Phe Ser Tyr Ser Leu Gly Ala Ile Cys Pro Lys His
385 390 395 400

tgc aag gtg ccc cat ggc ctc ttc cag ttc ttc ttc tgg atc ggc tac 1248
Cys Lys Val Pro His Gly Leu Phe Gln Phe Phe Phe Trp Ile Gly Tyr
405 410 415

tgc aac agc tca ctg aac cct gtt atc tac acc atc ttc aac cag gac 1296
Cys Asn Ser Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn Gln Asp
420 425 430

ttc cgc cgt gcc ttc cgg agg atc ctg tgc cgc ccg tgg acc cag acg 1344
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435 440 445

gcc tgg tga 1353
Ala Trp
450

<210> 23
<211> 450
<212> PRT
<213> Homo sapiens

<400> 23

Met Asp His Gln Asp Pro Tyr Ser Val Gln Ala Thr Ala Ala Ile Ala
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Ala Ala Ile Thr Phe Leu Ile Leu Phe Thr Ile Phe Gly Asn Ala Leu
20 25 30

Val Ile Leu Ala Val Leu Thr Ser Arg Ser Leu Arg Ala Pro Gln Asn
35 40 45

Leu Phe Leu Val Ser Leu Ala Ala Ala Asp Ile Leu Val Ala Thr Leu
50 55 60

Ile Ile Pro Phe Ser Leu Ala Asn Glu Leu Leu Gly Tyr Trp Tyr Phe
 65 70 75 80

Arg Arg Thr Trp Cys Glu Val Tyr Leu Ala Leu Asp Val Leu Phe Cys
 85 90 95

Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Trp
 100 105 110

Ala Val Ser Arg Ala Leu Glu Tyr Asn Ser Lys Arg Thr Pro Arg Arg
 115 120 125

Ile Lys Cys Ile Ile Leu Thr Val Trp Leu Ile Ala Ala Val Ile Ser
 130 135 140

Leu Pro Pro Leu Ile Tyr Lys Gly Asp Gln Gly Pro Gln Pro Arg Gly
 145 150 155 160

Arg Pro Gln Cys Lys Leu Asn Gln Glu Ala Trp Tyr Ile Leu Ala Ser
 165 170 175

Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met Ile Leu Val Tyr
 180 185 190

Leu Arg Ile Tyr Leu Ile Ala Lys Arg Ser Asn Arg Arg Gly Pro Arg
 195 200 205

Ala Lys Gly Gly Pro Gly Gln Gly Glu Ser Lys Gln Pro Arg Pro Asp
 210 215 220

His Gly Gly Ala Leu Ala Ser Ala Lys Leu Pro Ala Leu Ala Ser Val
 225 230 235 240

Ala Ser Ala Arg Glu Val Asn Gly His Ser Lys Ser Thr Gly Glu Lys
 245 250 255

Glu Glu Gly Glu Thr Pro Glu Asp Thr Gly Thr Arg Ala Leu Pro Pro
 260 265 270

Ser Trp Ala Ala Leu Pro Asn Ser Gly Gln Gly Gln Lys Glu Gly Val
 275 280 285

Cys Gly Ala Ser Pro Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu
 290 295 300

Glu Glu Glu Glu Glu Cys Glu Pro Gln Ala Val Pro Val Ser Pro Ala
 305 310 315 320

Ser Ala Cys Ser Pro Pro Leu Gln Gln Pro Gln Gly Ser Arg Val Leu
 325 330 335

Ala Thr Leu Arg Gly Gln Val Leu Leu Gly Arg Gly Val Gly Ala Ile
 340 345 350

Gly Gly Gln Trp Trp Arg Arg Arg Ala His Val Thr Arg Glu Lys Arg
 355 360 365

Phe Thr Phe Val Leu Ala Val Val Ile Gly Val Phe Val Leu Cys Trp
 370 375 380

Phe Pro Phe Phe Phe Ser Tyr Ser Leu Gly Ala Ile Cys Pro Lys His
 385 390 395 400

Cys Lys Val Pro His Gly Leu Phe Gln Phe Phe Phe Trp Ile Gly Tyr
 405 410 415

Cys Asn Ser Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn Gln Asp
 420 425 430

Phe Arg Arg Ala Phe Arg Arg Ile Leu Cys Arg Pro Trp Thr Gln Thr
 435 440 445

Ala Trp
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<210> 24
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR primer

<400> 24
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20

<210> 25

<211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Snapshot primer

 <400> 25
 tggcactgcc tggggttca 19

 <210> 26
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Sequencing primer

 <400> 26
 tcaggtcttc tcccagca 18

 <210> 27
 <211> 619
 <212> DNA
 <213> Homo sapiens

 <400> 27
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 tgactaacac atagctagta agatttcttg tcacttacga caaagacatg aattttctcc 180
 atcctaacat gactgataca gtgtctctta tttagactat ctcaagttagt ctggctgtgc 240
 ttgtcctttt tcccacctcc ctcgctgtgc ctgaccctct cttctttcca caggttctca 300
 ggcaagagcc acctgctatt gccgaaccgg ccgttgtgct acccgtgagt ccctctccgg 360
 ggtgtgtgaa atcagtggcc gcctctacag actctgctgt cgctgagctt cctagataga 420
 aaccaaagca gtgcaagatt cagttcaagg tcctgaaaaa agaaaaacat ttactctgt 480
 gtaccttggtg tcttttctaaa tttctctctc caaagtaaag ttcaagcatt aaacttagtg 540
 tgtttgacct ttttaatttt cttttctttt tccttttttt tcttttgctt tgttatatgg 600
 tggtttggtat ggttccttt 619

 <210> 28
 <211> 619
 <212> DNA
 <213> Homo sapiens

<400> 28
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 tgactaacac atagctagta agatttcttg tcacttacga caaagacatg aattttctcc 180
 atcctaacat gactgataca gtgtctctta tttagactat ctgagttagt ctggctgtgc 240
 ttgtcctttt tcccacctcc ctgctgtgc ctgacctct cttctttcca caggttctca 300
 ggcaagagcc acctgctatt gccgaaccgg ccgttggtgt acccgtgagt ccctctccgg 360
 ggtgtgtgaa atcagtggcc gcctctacag actctgctgt cgctgagctt cctagataga 420
 aaccaaagca gtgcaagatt cagttcaagg tcctgaaaaa agaaaaacat ttactctgt 480
 gtaccttggtg tctttctaaa tttctctctc caaaataaag ttcaagcatt aaacttagtg 540
 tgtttgacct ttttaatttt cttttctttt tccctttttt tcttttgctt tggttatatgg 600
 tggtttgtat gggttccttt 619

<210> 29
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR primer

<400> 29
 ggatgaagca gaatgaaga 19

<210> 30
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR primer

<400> 30
 aaaggaacca tacaaacca 19

<210> 31
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Sequencing primer

<400> 31

gttagtcttg ctgtgctt 18

<210> 32
 <211> 1052
 <212> DNA
 <213> Homo sapiens

<400> 32
 gggctactga gtttggtgaa aagataagac tcctgaaaat tctattgatt ctcttttgaa 60
 cttcttttctt aaattagttt tatgatggac ttggctctca ttggtatttc ccaagattat 120
 ggagatggga tagtgatgtc tgacaagtac ctaagatgct aagttgaagg tctaaaattc 180
 catcctaaaa gcaaataatt actctatcat ctacgtgcc tttgcttctt aaagttactc 240
 aaggaaggca gactaaacag gaaatttact ttggattcaa gaggggcata gagacgctct 300
 cagcctgccc atttgccctt atcaacattc ctaaactctg ggcttaaaat gtagtatgag 360
 taaactctct cttagtctat ccatctccca ctagcagttt taacatcatc tctagttatt 420
 aaccttggt caatggcttt ctctctttt tttatacaga atttattggc ttgagacgct 480
 gtttaaatggg tttggggaga tgcagggatc actgcaatgt ggatgaaaaa gagatacaga 540
 aatgcaagat gaaaaaatgt tgtgttgac caaaagtgg taaattgatt aaaaactacc 600
 tgcaatatgg aacaccaa atgtacttaatg aagacgtcca agaaatgcta aaacctgcca 660
 agaattctag tgctgtgata caaagaaaac atattttatc tgttctcccc caaatcaaaa 720
 gcactagctt ttttgcta atccaactttg tcatcattcc aaatgccacc cctatgaact 780
 ctgccaccat cagcactatg accccaggac agatcacata cactgctact tctaccaaga 840
 gtaacaccaa agaaagcaga gattctgcca ctgcctcgcc accaccagca ccacctccac 900
 caaacatact gccaacacca tcactggagc tagaggaagc agaagagcag taatgtggat 960
 ctttccctta aaactccaag ttctctctta tttttgctat ctataaaatg acatagaact 1020
 gtttcctctg tcatcagtca ttcaataaac ac 1052

<210> 33
 <211> 1049
 <212> DNA
 <213> Homo sapiens

<400> 33
 gggctactga gtttggtgaa aagataagac tcctgaaaat tctattgatt ctcttttgaa 60
 cttcttttctt aaattagttt tatgatggac ttggctctca ttggtatttc ccaagattat 120

ggagatggga tagtgatgtc tgacaagtac ctaagatgct aagttgaagg tctaaaattc	180
catcctaaaa gcaaataatt actctatcat ctacgtgccc tttgcttctt aaagttactc	240
aaggaaggca gactaaacag gaaatttact ttggattcaa gaggggcata gagacgctct	300
cagcctgccc atttgccttc atcaacattc ctaaactg ggcttaaaat gtagtatgag	360
taaactctct cttagtctat ccatctccca ctagcagttt taacatcatc tctagttatt	420
aaccttggct caatggcttt ctcttttttt atacagaatt tattggcttg agacgctgtt	480
taatgggttt ggggagatgc agggatcact gcaatgtgga tgaaaaagag atacagaaat	540
gcaagatgaa aaaatgttgt gttggaccaa aagtggttaa attgattaaa aactacctgc	600
aatatggaac accaaatgta cttaatgaag acgtccaaga aatgctaaaa cctgccaaga	660
attctagtgc tgtgatacaa agaaaacata ttttatctgt tctcccccaa atcaaaagca	720
ctagcttttt tgctaataacc aactttgtca tcattccaaa tgccaccctt atgaactctg	780
ccaccatcag cactatgacc ccaggacaga tcacatacac tgctacttct accaagagta	840
acaccaaaga aagcagagat tctgccactg cctcgccacc accagcacca cctccaccaa	900
acatactgcc aacaccatca ctggagctag aggaagcaga agagcagtaa tgtggatctt	960
tcccttaaaa ctccaagttc ctctctattt ttgctatcta taaaatgaca tagaactgtt	1020
tcctctgtca tcagtcattc aataaacac	1049

<210> 34
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR primer

<400> 34	
ggctactgag tttggtga	18

<210> 35
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR primer

<400> 35	
gtgtttattg aatgactgat g	21

<210> 36
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Sequencing primer

<400> 36
 caaggaaggc agactaaa 18

<210> 37
 <211> 552
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(552)
 <223> Coding sequence for the variant human DEFB129 gene

<400> 37
 atg aag ctc ctt ttt cct atc ttt gcc agc ctc atg cta cag tac cag 48
 Met Lys Leu Leu Phe Pro Ile Phe Ala Ser Leu Met Leu Gln Tyr Gln
 1 5 10 15

gtg aac aca gaa ttt att ggc ttg aga cgc tgt tta atg ggt ttg ggg 96
 Val Asn Thr Glu Phe Ile Gly Leu Arg Arg Cys Leu Met Gly Leu Gly
 20 25 30

aga tgc agg gat cac tgc aat gtg gat gaa aaa gag ata cag aaa tgc 144
 Arg Cys Arg Asp His Cys Asn Val Asp Glu Lys Glu Ile Gln Lys Cys
 35 40 45

aag atg aaa aaa tgt tgt gtt gga cca aaa gtg gtt aaa ttg att aaa 192
 Lys Met Lys Lys Cys Cys Val Gly Pro Lys Val Val Lys Leu Ile Lys
 50 55 60

aac tac ctg caa tat gga aca cca aat gta ctt aat gaa gac gtc caa 240
 Asn Tyr Leu Gln Tyr Gly Thr Pro Asn Val Leu Asn Glu Asp Val Gln
 65 70 75 80

gaa atg cta aaa cct gcc aag aat tct agt gct gtg ata caa aga aaa 288
 Glu Met Leu Lys Pro Ala Lys Asn Ser Ser Ala Val Ile Gln Arg Lys
 85 90 95

cat att tta tct gtt ctc ccc caa atc aaa agc act agc ttt ttt gct 336
 His Ile Leu Ser Val Leu Pro Gln Ile Lys Ser Thr Ser Phe Phe Ala
 100 105 110

aat acc aac ttt gtc atc att cca aat gcc acc cct atg aac tct gcc 384
 Asn Thr Asn Phe Val Ile Ile Pro Asn Ala Thr Pro Met Asn Ser Ala
 115 120 125

acc atc agc act atg acc cca gga cag atc aca tac act gct act tct 432
 Thr Ile Ser Thr Met Thr Pro Gly Gln Ile Thr Tyr Thr Ala Thr Ser

130	135	140	
acc aag agt aac acc aaa gaa agc aga gat tct gcc act gcc tcg cca			480
Thr Lys Ser Asn Thr Lys Glu Ser Arg Asp Ser Ala Thr Ala Ser Pro			
145	150	155	160
cca cca gca cca cct cca cca aac ata ctg cca aca cca tca ctg gag			528
Pro Pro Ala Pro Pro Pro Pro Asn Ile Leu Pro Thr Pro Ser Leu Glu			
	165	170	175
cta gag gaa gca gaa gag cag taa			552
Leu Glu Glu Ala Glu Glu Gln			
	180		

<210> 38
 <211> 183
 <212> PRT
 <213> Homo sapiens

<400> 38

Met Lys Leu Leu Phe Pro Ile Phe Ala Ser Leu Met Leu Gln Tyr Gln
1 5 10 15

Val Asn Thr Glu Phe Ile Gly Leu Arg Arg Cys Leu Met Gly Leu Gly
20 25 30

Arg Cys Arg Asp His Cys Asn Val Asp Glu Lys Glu Ile Gln Lys Cys
35 40 45

Lys Met Lys Lys Cys Cys Val Gly Pro Lys Val Val Lys Leu Ile Lys
50 55 60

Asn Tyr Leu Gln Tyr Gly Thr Pro Asn Val Leu Asn Glu Asp Val Gln
65 70 75 80

Glu Met Leu Lys Pro Ala Lys Asn Ser Ser Ala Val Ile Gln Arg Lys
85 90 95

His Ile Leu Ser Val Leu Pro Gln Ile Lys Ser Thr Ser Phe Phe Ala
100 105 110

Asn Thr Asn Phe Val Ile Ile Pro Asn Ala Thr Pro Met Asn Ser Ala
115 120 125

Thr Ile Ser Thr Met Thr Pro Gly Gln Ile Thr Tyr Thr Ala Thr Ser
130 135 140

Thr Lys Ser Asn Thr Lys Glu Ser Arg Asp Ser Ala Thr Ala Ser Pro
 145 150 155 160

Pro Pro Ala Pro Pro Pro Pro Asn Ile Leu Pro Thr Pro Ser Leu Glu
 165 170 175

Leu Glu Glu Ala Glu Glu Gln
 180

<210> 39
 <211> 552
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(552)
 <223> Coding sequence for the human DEFB129 gene

<400> 39
 atg aag ctc ctt ttt cct atc ttt gcc agc ctc atg cta cag tac cag 48
 Met Lys Leu Leu Phe Pro Ile Phe Ala Ser Leu Met Leu Gln Tyr Gln
 1 5 10 15
 gtg aac aca gaa ttt att ggc ttg aga cgc tgt tta atg ggt ttg ggg 96
 Val Asn Thr Glu Phe Ile Gly Leu Arg Arg Cys Leu Met Gly Leu Gly
 20 25 30
 aga tgc agg gat cac tgc aat gtg gat gaa aaa gag ata cag aaa tgc 144
 Arg Cys Arg Asp His Cys Asn Val Asp Glu Lys Glu Ile Gln Lys Cys
 35 40 45
 aag atg aaa aaa tgt tgt gtt gga cca aaa gtg gtt aaa ttg att aaa 192
 Lys Met Lys Lys Cys Cys Val Gly Pro Lys Val Val Lys Leu Ile Lys
 50 55 60
 aac tac cta caa tat gga aca cca aat gta ctt aat gaa gac gtc caa 240
 Asn Tyr Leu Gln Tyr Gly Thr Pro Asn Val Leu Asn Glu Asp Val Gln
 65 70 75 80
 gaa atg cta aaa cct gcc aag aat tct agt gct gtg ata caa aga aaa 288
 Glu Met Leu Lys Pro Ala Lys Asn Ser Ser Ala Val Ile Gln Arg Lys
 85 90 95
 cat att tta tct gtt ctc ccc caa atc aaa agc act agc ttt ttt gct 336
 His Ile Leu Ser Val Leu Pro Gln Ile Lys Ser Thr Ser Phe Phe Ala
 100 105 110
 aat acc aac ttt gtc atc att cca aat gcc acc cct atg aac tct gcc 384
 Asn Thr Asn Phe Val Ile Ile Pro Asn Ala Thr Pro Met Asn Ser Ala
 115 120 125
 acc atc agc act atg acc cca gga cag atc aca tac act gct act tct 432

Thr	Ile	Ser	Thr	Met	Thr	Pro	Gly	Gln	Ile	Thr	Tyr	Thr	Ala	Thr	Ser		
130						135					140						
acc	aag	agt	aac	acc	aaa	gaa	agc	aga	gat	tct	gcc	act	gcc	tcg	cca	480	
Thr	Lys	Ser	Asn	Thr	Lys	Glu	Ser	Arg	Asp	Ser	Ala	Thr	Ala	Ser	Pro		
145					150				155						160		
cca	cca	gca	cca	cct	cca	cca	aac	ata	ctg	cca	aca	cca	tca	ctg	gag	528	
Pro	Pro	Ala	Pro	Pro	Pro	Pro	Asn	Ile	Leu	Pro	Thr	Pro	Ser	Leu	Glu		
				165					170					175			
cta	gag	gaa	gca	gaa	gag	cag	taa									552	
Leu	Glu	Glu	Ala	Glu	Glu	Gln											
			180														

<210> 40
 <211> 183
 <212> PRT
 <213> Homo sapiens

<400> 40

Met	Lys	Leu	Leu	Phe	Pro	Ile	Phe	Ala	Ser	Leu	Met	Leu	Gln	Tyr	Gln
1				5					10					15	

Val	Asn	Thr	Glu	Phe	Ile	Gly	Leu	Arg	Arg	Cys	Leu	Met	Gly	Leu	Gly
			20					25					30		

Arg	Cys	Arg	Asp	His	Cys	Asn	Val	Asp	Glu	Lys	Glu	Ile	Gln	Lys	Cys
		35					40					45			

Lys	Met	Lys	Lys	Cys	Cys	Val	Gly	Pro	Lys	Val	Val	Lys	Leu	Ile	Lys
	50					55					60				

Asn	Tyr	Leu	Gln	Tyr	Gly	Thr	Pro	Asn	Val	Leu	Asn	Glu	Asp	Val	Gln
65					70					75					80

Glu	Met	Leu	Lys	Pro	Ala	Lys	Asn	Ser	Ser	Ala	Val	Ile	Gln	Arg	Lys
				85					90					95	

His	Ile	Leu	Ser	Val	Leu	Pro	Gln	Ile	Lys	Ser	Thr	Ser	Phe	Phe	Ala
			100					105					110		

Asn	Thr	Asn	Phe	Val	Ile	Ile	Pro	Asn	Ala	Thr	Pro	Met	Asn	Ser	Ala
		115					120					125			

Thr	Ile	Ser	Thr	Met	Thr	Pro	Gly	Gln	Ile	Thr	Tyr	Thr	Ala	Thr	Ser
130						135					140				

Thr Lys Ser Asn Thr Lys Glu Ser Arg Asp Ser Ala Thr Ala Ser Pro
 145 150 155 160

Pro Pro Ala Pro Pro Pro Pro Asn Ile Leu Pro Thr Pro Ser Leu Glu
 165 170 175

Leu Glu Glu Ala Glu Glu Gln
 180

<210> 41
 <211> 372
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(372)
 <223> Coding sequence for the variant human DEFB118 gene

<400> 41
 atg aaa ctc ctg ctg ctg gct ctt cct atg ctt gtg ctc cta ccc caa 48
 Met Lys Leu Leu Leu Leu Ala Leu Pro Met Leu Val Leu Leu Pro Gln
 1 5 10 15
 gtg atc cca gcc tat agt ggt gaa aaa aaa tgc tgg aac aga tca ggg 96
 Val Ile Pro Ala Tyr Ser Gly Glu Lys Lys Cys Trp Asn Arg Ser Gly
 20 25 30
 cac cgc agg aaa caa tgc aaa gat gga gaa gca gtg aaa gat aca tgc 144
 His Arg Arg Lys Gln Cys Lys Asp Gly Glu Ala Val Lys Asp Thr Cys
 35 40 45
 aaa aat ctt cga gct tgc tgc att cca tcc aat gaa gac cac agg cga 192
 Lys Asn Leu Arg Ala Cys Cys Ile Pro Ser Asn Glu Asp His Arg Arg
 50 55 60
 gtt cct gcg aca tct ccc aca ccc ttg agt gac tca aca cca gga att 240
 Val Pro Ala Thr Ser Pro Thr Pro Leu Ser Asp Ser Thr Pro Gly Ile
 65 70 75 80
 att gat gat att tta aca gta agg ttc acg aca gac tac ttt gaa gta 288
 Ile Asp Asp Ile Leu Thr Val Arg Phe Thr Thr Asp Tyr Phe Glu Val
 85 90 95
 agc agc aag aaa gat atg gtt gaa gag tct gag gcg gga agg gga act 336
 Ser Ser Lys Lys Asp Met Val Glu Glu Ser Glu Ala Gly Arg Gly Thr
 100 105 110
 gag acc tct ctt cca aat gtt cac cat agc tca tga 372
 Glu Thr Ser Leu Pro Asn Val His His Ser Ser
 115 120

<210> 42
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 42

Met Lys Leu Leu Leu Leu Ala Leu Pro Met Leu Val Leu Leu Pro Gln
 1 5 10 15

Val Ile Pro Ala Tyr Ser Gly Glu Lys Lys Cys Trp Asn Arg Ser Gly
 20 25 30

His Arg Arg Lys Gln Cys Lys Asp Gly Glu Ala Val Lys Asp Thr Cys
 35 40 45

Lys Asn Leu Arg Ala Cys Cys Ile Pro Ser Asn Glu Asp His Arg Arg
 50 55 60

Val Pro Ala Thr Ser Pro Thr Pro Leu Ser Asp Ser Thr Pro Gly Ile
 65 70 75 80

Ile Asp Asp Ile Leu Thr Val Arg Phe Thr Thr Asp Tyr Phe Glu Val
 85 90 95

Ser Ser Lys Lys Asp Met Val Glu Glu Ser Glu Ala Gly Arg Gly Thr
 100 105 110

Glu Thr Ser Leu Pro Asn Val His His Ser Ser
 115 120

<210> 43
 <211> 372
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(372)
 <223> Coding sequence of the human DEFB118 gene

<400> 43

atg aaa ctc ctg ctg ctg gct ctt cct atg ctt gtg ctc cta ccc caa 48
 Met Lys Leu Leu Leu Leu Ala Leu Pro Met Leu Val Leu Leu Pro Gln
 1 5 10 15

gtg atc cca gcc tat agt ggt gaa aaa aaa tgc tgg aac aga tca ggg 96
 Val Ile Pro Ala Tyr Ser Gly Glu Lys Lys Cys Trp Asn Arg Ser Gly

20	25	30	
cac tgc agg aaa caa tgc aaa gat gga gaa gca gtg aaa gat aca tgc His Cys Arg Lys Gln Cys Lys Asp Gly Glu Ala Val Lys Asp Thr Cys 35 40 45			144
aaa aat ctt cga gct tgc tgc att cca tcc aat gaa gac cac agg cga Lys Asn Leu Arg Ala Cys Cys Ile Pro Ser Asn Glu Asp His Arg Arg 50 55 60			192
gtt cct gcg aca tct ccc aca ccc ttg agt gac tca aca cca gga att Val Pro Ala Thr Ser Pro Thr Pro Leu Ser Asp Ser Thr Pro Gly Ile 65 70 75 80			240
att gat gat att tta aca gta agg ttc acg aca gac tac ttt gaa gta Ile Asp Asp Ile Leu Thr Val Arg Phe Thr Thr Asp Tyr Phe Glu Val 85 90 95			288
agc agc aag aaa gat atg gtt gaa gag tct gag gcg gga agg gga act Ser Ser Lys Lys Asp Met Val Glu Glu Ser Glu Ala Gly Arg Gly Thr 100 105 110			336
gag acc tct ctt cca aat gtt cac cat agc tca tga Glu Thr Ser Leu Pro Asn Val His His Ser Ser 115 120			372

<210> 44
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 44

Met Lys Leu Leu Leu Leu Ala Leu Pro Met Leu Val Leu Leu Pro Gln 1 5 10 15
Val Ile Pro Ala Tyr Ser Gly Glu Lys Lys Cys Trp Asn Arg Ser Gly 20 25 30
His Cys Arg Lys Gln Cys Lys Asp Gly Glu Ala Val Lys Asp Thr Cys 35 40 45
Lys Asn Leu Arg Ala Cys Cys Ile Pro Ser Asn Glu Asp His Arg Arg 50 55 60
Val Pro Ala Thr Ser Pro Thr Pro Leu Ser Asp Ser Thr Pro Gly Ile 65 70 75 80
Ile Asp Asp Ile Leu Thr Val Arg Phe Thr Thr Asp Tyr Phe Glu Val 85 90 95

Ser Ser Lys Lys Asp Met Val Glu Glu Ser Glu Ala Gly Arg Gly Thr
100 105 110

Glu Thr Ser Leu Pro Asn Val His His Ser Ser
115 120

<210> 45
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 45
aggttgagta tttgccagac 20

<210> 46
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 46
aggacagggg tgagtgata 19

<210> 47
<211> 246
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(246)
<223> Coding sequence for the variant human DEFB126 gene

<400> 47
atg aag tcc cta ctg ttc acc ctt gca gtt ttt atg ctc ctg gcc caa 48
Met Lys Ser Leu Leu Phe Thr Leu Ala Val Phe Met Leu Leu Ala Gln
1 5 10 15

ttg gtc tca ggt aat tgg tat gtg aaa aag tgt cta aac gac gtt gga 96
Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys Leu Asn Asp Val Gly
20 25 30

att tgc aag aag aag tgc aaa cct gaa gag atg cat gta aag aat ggt 144
Ile Cys Lys Lys Lys Cys Lys Pro Glu Glu Met His Val Lys Asn Gly
35 40 45

tgg gca atg tgc ggc aaa ggg act gct gtg ttc cag ctg aca gac gtg 192

Trp Ala Met Cys Gly Lys Gly Thr Ala Val Phe Gln Leu Thr Asp Val
50 55 60

cta att atc ctg ttt tct gtg tcc aga caa aga cta caa gaa ttt caa 240
Leu Ile Ile Leu Phe Ser Val Ser Arg Gln Arg Leu Gln Glu Phe Gln
65 70 75 80

cag taa 246
Gln

<210> 48
<211> 81
<212> PRT
<213> Homo sapiens

<400> 48

Met Lys Ser Leu Leu Phe Thr Leu Ala Val Phe Met Leu Leu Ala Gln
1 5 10 15

Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys Leu Asn Asp Val Gly
20 25 30

Ile Cys Lys Lys Lys Cys Lys Pro Glu Glu Met His Val Lys Asn Gly
35 40 45

Trp Ala Met Cys Gly Lys Gly Thr Ala Val Phe Gln Leu Thr Asp Val
50 55 60

Leu Ile Ile Leu Phe Ser Val Ser Arg Gln Arg Leu Gln Glu Phe Gln
65 70 75 80

Gln

<210> 49
<211> 336
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(336)
<223> Coding sequence of the human DEFB126 gene

<400> 49
atg aag tcc cta ctg ttc acc ctt gca gtt ttt atg ctc ctg gcc caa 48
Met Lys Ser Leu Leu Phe Thr Leu Ala Val Phe Met Leu Leu Ala Gln
1 5 10 15

ttg gtc tca ggt aat tgg tat gtg aaa aag tgt cta aac gac gtt gga	96
Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys Leu Asn Asp Val Gly	
20 25 30	

att tgc aag aag aag tgc aaa cct gaa gag atg cat gta aag aat ggt	144
Ile Cys Lys Lys Lys Cys Lys Pro Glu Glu Met His Val Lys Asn Gly	
35 40 45	

tgg gca atg tgc ggc aaa caa agg gac tgc tgt gtt cca gct gac aga	192
Trp Ala Met Cys Gly Lys Gln Arg Asp Cys Cys Val Pro Ala Asp Arg	
50 55 60	

cgt gct aat tat cct gtt ttc tgt gtc cag aca aag act aca aga att	240
Arg Ala Asn Tyr Pro Val Phe Cys Val Gln Thr Lys Thr Thr Arg Ile	
65 70 75 80	

tca aca gta aca gca aca aca gca aca aca act ttg atg atg act act	288
Ser Thr Val Thr Ala Thr Thr Ala Thr Thr Thr Leu Met Met Thr Thr	
85 90 95	

gct tcg atg tct tcg atg gct cct acc ccc gtt tct ccc act ggt tga	336
Ala Ser Met Ser Ser Met Ala Pro Thr Pro Val Ser Pro Thr Gly	
100 105 110	

<210> 50
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 50

Met Lys Ser Leu Leu Phe Thr Leu Ala Val Phe Met Leu Leu Ala Gln
1 5 10 15

Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys Leu Asn Asp Val Gly
20 25 30

Ile Cys Lys Lys Lys Cys Lys Pro Glu Glu Met His Val Lys Asn Gly
35 40 45

Trp Ala Met Cys Gly Lys Gln Arg Asp Cys Cys Val Pro Ala Asp Arg
50 55 60

Arg Ala Asn Tyr Pro Val Phe Cys Val Gln Thr Lys Thr Thr Arg Ile
65 70 75 80

Ser Thr Val Thr Ala Thr Thr Ala Thr Thr Thr Leu Met Met Thr Thr
85 90 95

Ala Ser Met Ser Ser Met Ala Pro Thr Pro Val Ser Pro Thr Gly
100 105 110

<210> 51
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 51
aatggtgaga aagatgacag 20

<210> 52
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 52
gttgaatgga gggaaagt 18

<210> 53
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequencing primer

<400> 53
gtaggtatatt atgattag 18

<210> 54
<211> 334
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(333)
<223> Coding sequence for the variant human DEFB126 gene

<400> 54
atg aag tcc cta ctg ttc acc ctt gca gtt ttt atg ctc ctg gcc caa 48
Met Lys Ser Leu Leu Phe Thr Leu Ala Val Phe Met Leu Leu Ala Gln
1 5 10 15

ttg gtc tca ggt aat tgg tat gtg aaa aag tgt cta aac gac gtt gga 96
Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys Leu Asn Asp Val Gly

20										25					30					
att tgc aag aag aag tgc aaa cct gaa gag atg cat gta aag aat ggt	144																			
Ile Cys Lys Lys Lys Cys Lys Pro Glu Glu Met His Val Lys Asn Gly																				
35 40 45																				
tgg gca atg tgc ggc aaa caa agg gac tgc tgt gtt cca gct gac aga	192																			
Trp Ala Met Cys Gly Lys Gln Arg Asp Cys Cys Val Pro Ala Asp Arg																				
50 55 60																				
cgt gct aat tat cct gtt ttc tgt gtc cag aca aag act aca aga att	240																			
Arg Ala Asn Tyr Pro Val Phe Cys Val Gln Thr Lys Thr Thr Arg Ile																				
65 70 75 80																				
tca aca gta aca gca aca aca gca aca aca act ttg atg atg act act	288																			
Ser Thr Val Thr Ala Thr Thr Ala Thr Thr Thr Leu Met Met Thr Thr																				
85 90 95																				
gct tcg atg tct tcg atg gct cct acc cgt ttc tcc cac tgg ttg a	334																			
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Ile Cys Lys Lys Lys Cys Lys Pro Glu Glu Met His Val Lys Asn Gly	
35 40 45	
Trp Ala Met Cys Gly Lys Gln Arg Asp Cys Cys Val Pro Ala Asp Arg	
50 55 60	
Arg Ala Asn Tyr Pro Val Phe Cys Val Gln Thr Lys Thr Thr Arg Ile	
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